

1 GCTGGATGGTGGACTCAGAGACCAATAAAAATAAACTGCTTGAACATCCTTTGACTGGTT
 -----+-----+-----+-----+-----+-----+ 60
 CGACCTACCACCTGAGTCTCIGGTTATTTTATTTGACGAACTTGTAGGAACTGACCAA

 61 AGCCAGTTGCTGATGTATATICAAGATGAGTGGATTAGGAGAAAACCTTGGATCCACTGGC
 -----+-----+-----+-----+-----+-----+ 120
 TCGGTCAACGACTACATATAAGTTCTACTCACCTAATCCTCTTTTGAACCTAGGTGACCG

 M S G L G E N L D P L A -

 121 CAGTGATTACGAAAACGCAATTGCCATGTGATACTCCAGGACAAGGTCTTACCTGCAG
 -----+-----+-----+-----+-----+-----+ 180
 GTCACTAAGTGCTTTTGCCTTTAACGGTACACTATGAGGTCCTGTTCCAGAATGGACGTC

 S D S R K R K L P C D T P G Q G L T C S -

 181 TGGTGAAAAACGGAGACGGGAGCAGGAAAGTAAATATATTGAAGAATTGGCTGAGCTGAT
 -----+-----+-----+-----+-----+-----+ 240
 ACCACTTTTTGCCTCTGCCCTCGTCCCTTTCATTTATATAACTTCTTAACCGACTCGACTA

 G E K R R R E Q E S K Y I E E L A E L I -

 241 ATCTGCCAATCTTAGTGATAITGACAATTTCAATGTCAAACCAGATAAATGTGCGATTTT
 -----+-----+-----+-----+-----+-----+ 300
 TAGACGGTTAGAATCACTATAACTGTAAAGTTACAGTTTGGTCTATTTACACGCTAAAA

 S A N L S D I D N F N V K P D K C A I L -

 301 AAAGGAAACAGTAAGACAGATACGTCAAATAAAAGAGCAAGGAAAAACTATTTCCAATGA
 -----+-----+-----+-----+-----+-----+ 360
 TTTCTTTTGTCAATCTGTCTATGCAGTTTATTTTCTCGTTCCTTTTGTATAAAGGTTACT

 K E T V R Q I R Q I K E Q G K T I S N D -

 361 TGATGATGTTCAAAAAGCCGATGTATCTTCTACAGGGCAGGGAGTTATTGATAAAGACTC
 -----+-----+-----+-----+-----+-----+ 420
 ACTACTACAAGTTTTTCGGCTACATAGAAGATGTCCCGTCCCTCAATAACTATTTCTGAG

 D D V Q K A D V S S T G Q G V I D K D S -

 421 CTTAGGACCGCTTTTACTTCAGGCATTGGATGGTTTCTTATTTGTGGTGAATCGAGAGGC
 -----+-----+-----+-----+-----+-----+ 480
 GAATCCTGGCGAAAATGAAGTCCGTAACCTACCAAAGGATAAACACCACTTAGCTCTCCG

 L G P L L L Q A L D G F L F V V N R E A -

 481 AAACATTGTATTTGTATCAGAAAATGTCACACAATACCTGCAATATAAGCAAGAGGACCT
 -----+-----+-----+-----+-----+-----+ 540
 TTTGTAACATAAACATAGTCTTTTACAGTGTGTTATGGACGTTATATTCGTTCTCTTGA

 N I V F V S E N V T Q Y L Q Y K Q E D L -

 541 GGTTAACACAAGTGTTTACAATATCTTACATGAAGAAGACAGAAAGGATTTTCTTAAGAA
 -----+-----+-----+-----+-----+-----+ 600
 CCAATTGTGTTCACAAATGTIATAGAATGTACTTCTTCTGTCTTTCCTAAAAGAATTCTT

FIGURE 1

V N T S V Y N I L H E E D R K D F L K N -
 TTTACCAAATCTACAGTTAATGGAGTTTCCTGGACAAATGAGACCCAAAGACAAAAAG
 601 -----+-----+-----+-----+-----+ 660
 AAATGGTTTTAGATGTCAATTACCTCAAAGGACCTGTTTACTCTGGGTTTCTGTTTTTC
 L P K S T V N G V S W T N E T Q R Q K S -
 TCATACATTTAATTGCCGTATGTTGATGAAAACACCACATGATATTCTGGAAGACATAAA
 661 -----+-----+-----+-----+-----+ 720
 GGTATGTAAATTAACGGCATACAACTACTTTTGTGGTGTACTATAAGACCTTCTGTATTT
 H T F N C R M L M K T P H D I L E D I N -
 CGCCAGTCCTGAAATGCGCCAGAGATATGAAACAATGCAGTGCTTTGCCCTGTCTCAGCC
 721 -----+-----+-----+-----+-----+ 780
 GCGGTCAGGACTTTACGCGGTCTCTATACTTTGTTACGTCACGAAACGGGACAGAGTCGG
 A S P E M R Q R Y E T M Q C F A L S Q P -
 ACGAGCTATGATGGAGGAAGCGGAAGATTTGCAATCTTGTATGATCTGTGTGGCAGCCG
 781 -----+-----+-----+-----+-----+ 840
 TGCTCGATACTACCTCCTTCCCTTCTAAACGTTAGAACATACTAGACACACCGTGCGGC
 R A M M E E G E D L Q S C M I C V A R R -
 CATTACTACAGGAGAAAGAACATTTCCATCAAACCCTGAGAGCTTTATTACCAGACATGA
 841 -----+-----+-----+-----+-----+ 900
 GTAATGATGTCCTCTTTCTGTAAAGGTAGTTTGGGACTCTCGAAATAATGGTCTGTACT
 I T T G E R T F P S N P E S F I T R H D -
 TCTTTCAGGAAAGGTTGTCAATATAGATACAAATTCAGTACTGAGATCCTCCATGAGGCCTGG
 901 -----+-----+-----+-----+-----+ 960
 AGAAAGTCCTTTCCAACAGTTATATCTATGTTTAAGTGACTCTAGGAGGTACTCCGGACC
 L S G K V V N I D T N S L R S S M R P G -
 CTTTGAAGATATAATCCGAAGGTGTATTCAGAGATTTTTTAGTCTAAATGATGGGCAGTC
 961 -----+-----+-----+-----+-----+ 1020
 GAAACTTCTATATTAGGCTTCCACATAAGTCTCTAAAAAATCAGATTTACTACCCGTCAG
 F E D I I R R C I Q R F F S L N D G Q S -
 ATGGTCCCAGAAACGTCAGTATCAAGAAGCTTATCTTAATGGCCATGCAGAAACCCAGT
 1021 -----+-----+-----+-----+-----+ 1080
 TACCAGGGTCTTTGCAGTGATAGTTCTTCGAATAGAATTACCGGTACGTCTTTGGGGTCA
 W S Q K R H Y Q E A Y L N G H A E T P V -
 ATATCGATTCTCGTTGGCTGATGGAAGTATAGTGACTGCACAGACAAAAGCAAACCTTT
 1081 -----+-----+-----+-----+-----+ 1140
 TATAGCTAAGAGCAACCGACTACCTTGATATCACTGACGTGTCTGTTTTTCGTTTGAGAA
 Y R F S L A D G T I V T A Q T K S K L F -
 CCGAAATCCTGTAACAAATGATCGACATGGCTTTGTCTCAACCCACTTCCTTCAGAGAGA
 1141 -----+-----+-----+-----+-----+ 1200
 GGCTTTAGGACATTGTTTACTAGCTGTACCGAAACAGAGTTGGGTGAAGGAAGTCTCTCT
 R N P V T N D R H G F V S T H F L Q R E -

FIGURE 1A

ACAGAATGGATATAGACCAAAACCCAAATCCTGTTGGACAAGGGATTAGACCACCTATGGC
 1201 -----+-----+-----+-----+-----+-----+-----+ 1260
 TGTCTTACCTATATCTGGTTTGGGTTTAGGACAACCTGTTCCCTAATCTGGTGGATACCG
 Q N G Y R P N P N P V G Q G I R P P M A -
 TGGATGCAACAGTTCCGGTAGGCGGCATGAGTATGTGCGCCAAACCAAGGCTTACAGATGCC
 1261 -----+-----+-----+-----+-----+-----+-----+ 1320
 ACCTACGTTGTCAAGCCATCCGCCGTACTCATAACAGCGGTTTGGTTCCGAATGTCTACGG
 G C N S S V G G M S M S P N Q G L Q M P -
 GAGCAGCAGGGCCTATGGCTTGGCAGACCCTAGCACCACAGGGCAGATGAGTGGAGCTAG
 1321 -----+-----+-----+-----+-----+-----+-----+ 1380
 CTCGTCGTCCCGGATACCGAACCGTCTGGGATCGTGGTGTCCCGTCTACTCACCTCGATC
 S S R A Y G L A D P S T T G Q M S G A R -
 GTATGGGGGTTCCAGTAACAAGCTTCATTGACCCCTGGGGCCAGGCATGCAATCACCATC
 1381 -----+-----+-----+-----+-----+-----+-----+ 1440
 CATACCCCCAAGGTCATTGTATCGAAGTAAGTGGGGACCCGGTCCGTACGTTAGTGGTAG
 Y G G S S N I A S L T P G P G M Q S P S -
 TTCCTACCAGAACAACAATATGGGCTCAACATGAGTAGCCCCCACATGGGAGTCCTGG
 1441 -----+-----+-----+-----+-----+-----+-----+ 1500
 AAGGATGGTCTTGTGTTGATACCCGAGTTGTACTCATCGGGGGGTGTACCCTCAGGACC
 S Y Q N N N Y G L N M S S P P H G S P G -
 TCTTGCCCCAAACCAGCAGAAATATCATGATTTCTCCTCGTAATCGTGGGAGTCCAAAGAT
 1501 -----+-----+-----+-----+-----+-----+-----+ 1560
 AGAACGGGGTTTGGTTCGTCTATAGTACTAAAGAGGAGCATTAGCACCCCTCAGGTTTCTA
 L A P N Q Q N I M I S P R N R G S P K I -
 AGCCTCACATCAGTTTTCTCCTGTTGCAGGTGTGCACTCTCCCATGGCATCTTCTGGCAA
 1561 -----+-----+-----+-----+-----+-----+-----+ 1620
 TCGGAGTGTAGTCAAAAGAGGACAACGTCCACACGTGAGAGGGTACCGTAGAAGACCGTT
 A S H Q F S P V A G V H S P M A S S G N -
 TACTGGGAACCACAGCTTTTTCAGCAGCTCTCTCAGTGGCCCTGCAAGCCATCAGTGAAGG
 1621 -----+-----+-----+-----+-----+-----+-----+ 1680
 ATGACCCTTGGTGTGCAAAAGGTCGTGAGAGAGTCACGGGACGTTCCGGTAGTCACTTCC
 T G N H S F S S S S L S A L Q A I S E G -
 TGTGGGGACTTCCCTTTTATCTACTCTGTATCACCAGGCCCCAAATTGGATAACTCTCC
 1681 -----+-----+-----+-----+-----+-----+-----+ 1740
 ACACCCCTGAAGGGAAAATAGATGAGACAGTAGTGGTCCGGGGTTTAACCTATTGAGAGG
 V G T S L L S T L S S P G P K L D N S P -
 CAATATGAATATTACCCAACCAAGTAAAGTAAGCAATCAGGATTCCAAGAGTCCTCTGGG
 1741 -----+-----+-----+-----+-----+-----+-----+ 1800
 GTTATACTTATAATGGGTTGCTTCATTTTCATTCGTTAGTCCTAAGGTTCTCAGGAGACCC
 N M N I T Q P S K V S N Q D S K S P L G -
 CTTTTATTGCGACCAAAATCCAGTGGAGAGTTCAATGTGTGTCAGTCAAATAGCAGAGATCA

FIGURE 1B

1801 -----+-----+-----+-----+-----+-----+-----+ 1860
 GAAAATAACGCTGGTTTTAGGTCACCTCTCAAGTTACACAGTCAGTTTATCGTCTCTAGT
 F Y C D Q N P V E S S M C Q S N S R D H -
 -CTCAGTGACAAAGAAAGTAAAGGAGAGCAGTGTTGAGGGGGCAGAGAATCAAAGGGGTCC
 1861 -----+-----+-----+-----+-----+-----+-----+ 1920
 GGAGTCACTGTTTCTTTTCATTCTCTCGTCACAACCTCCCCCGTCTCTTAGTTTCCCCCAGG
 L S D K E S K E S S V E G A E N Q R G P -
 TTTGGAAAGCAAAGGTCATAA AAAATTACTGCAGTTACTTACCTGTTCTTCTGATGACCG
 1921 -----+-----+-----+-----+-----+-----+-----+ 1980
 AAACCTTTTCGTTTCCAGTATTTTAAATGACGTCAATGAATGGACAAGAAGACTACTGGC
 L E S K G H K K L L Q L L T C S S D D R -
 GGGTCATTCCCTCCTTGACCAACTCCCCCCTAGATTCAAGTTGTAAAGAATCTTCTGTTAG
 1981 -----+-----+-----+-----+-----+-----+-----+ 2040
 CCCAGTAAGGAGGAAGTGGTGGAGGGGGATCTAAGTTCAACATTCTTAGAAGACAATC
 G H S S L T N S P L D S S C K E S S V S -
 TGTCACCAGCCCCCTCTGGAGTCTCCTCCTCTACATCTGGAGGAGTATCCTCTACATCCAA
 2041 -----+-----+-----+-----+-----+-----+-----+ 2100
 ACAGTGGTCTGGGGAGACCTCAGAGGAGGAGATGTAGACCTCCTCATAGGAGATGTAGGTT
 V T S P S G V S S S T S G G V S S T S N -
 TATGCATGGGTCACTGTTACAAGAGAAGCACCGGATTTTGCACAAGTTGCTGCAGAATGG
 2101 -----+-----+-----+-----+-----+-----+-----+ 2160
 ATACGTACCCAGTGACAATGTCTCTTCGTGGCCTAAACGTGTTCAACGACGTCTTACC
 M H G S L L Q E K H R I L H K L L Q N G -
 GAATTCACCAGCTGAGGTAGCCAAGATTACTGCAGAAGCCACTGGGAAAGACACCAGCAG
 2161 -----+-----+-----+-----+-----+-----+-----+ 2220
 CTTAAGTGGTCTGACTCCATCGGTTCTAATGACGTCTTCGGTGACCCTTTCTGTGGTCTGTC
 N S P A E V A K I T A E A T G K D T S S -
 TATAACTTCTTGTGGGGACGCAATGTTGTCAAGCAGGAGCAGCTAAGTCCTAAGAAGAA
 2221 -----+-----+-----+-----+-----+-----+-----+ 2280
 ATATTGAAGAACACCCCTGCCTTTACAACAGTTCGTCCTCGTCGATTCAGGATTCTTCTT
 I T S C G D G N V V K Q E Q L S P K K K -
 GGAGAATAATGCACCTTCTTAGATACCTGCTGGACAGGGATGATCCTAGTGATGCACCTCTC
 2281 -----+-----+-----+-----+-----+-----+-----+ 2340
 CCTCTTATTACGTGAAGAATCTATGGACGACCTGTCCCTACTAGGATCACTACGTGAGAG
 E N N A L L R Y L L D R D D P S D A L S -
 TAAAGAACTACAGCCCCAAGTGAAGGAGTGGACAATAAAATGAGTCAGTGCACCAGCTC
 2341 -----+-----+-----+-----+-----+-----+-----+ 2400
 ATTTCTTGATGTCGGGGTTCACCTTCCTCACCTGTTATTTTACTCAGTCACGTGGTCT 37.3
 K E L Q P Q V E G V D N K M S Q C T S S -
 CACCATTCCCTAGCTCAAGTCAAGAGAAAGACCCTAAAATTAAGACAGAGACAAGTGAAGA
 2401 -----+-----+-----+-----+-----+-----+-----+ 2460
 GTGGTAAGGATCGAGTTCAGTCTCTTTCTGGGATTTTAATTCTGTCTCTGTTCACCTTCT

FIGURE 1C

T I P S S S Q E K D P K I K T E T S E E -
 2461 GGGATCTGGAGACTTGGATAATCTAGATGCTATTCTTGGTGATCTGACTAGTTCTGACTT
 -----+-----+-----+-----+-----+ 2520
 CCCTAGACCTCTGAACCTATTAGATCTACGATAAGAACCCTAGACTGATCAAGACTGAA
 G S G D L D N L D A I L G D L T S S D F -
 2521 TTACAATAATTCCATATCCTCAAATGGTAGTCATCTGGGGACTAAGCAACAGGTGTTTCA
 -----+-----+-----+-----+-----+ 2580
 AATGTTATTAAGGTATAGGAGTTTACCATCAGTAGACCCCTGATTTCGTTGTCCACAAAGT
 Y N N S I S S N G S H L G T K Q Q V F Q -
 2581 AGGAACTAATTCTCTGGGTTTGAAAAGTTCACAGTCTGTGCAGTCTATTTCGTCTCCATA
 -----+-----+-----+-----+-----+ 2640
 TCCTTGATTAAGAGACCCAACTTTTCAAGTGTGACACGTCAGATAAGCAGGAGGTAT
 G T N S L G L K S S Q S V Q S I R P P Y -
 2641 TAACCGAGCAGTGTCTCTGGATAGCCCTGTTTCTGTTGGCTCAAGTCCTCCAGTAAAAA
 -----+-----+-----+-----+-----+ 2700
 ATTGGCTCGTCAAGAGACCTATCGGGACAAAGACAACCGAGTTCAGGAGGTCATTTTTT
 N R A V S L D S P V S V G S S P P V K N -
 2701 ATCAGTGCTTTCCCATGTACCAAAGCAACCCATGTTGGGTGGGAATCCAAGAATGAT
 -----+-----+-----+-----+-----+ 2760
 ATAGTCACGAAAGGGGTACAATGGTTTCGTTGGGTACAACCCACCCTTAGGTTCTTACTA
 I S A F P M L P K Q P M L G G N P R M M -
 2761 GGATAGTCAGGAAAATTATGGCTCAAGTATGGGTGGGCCAAACCGAAATGTGACTGTGAC
 -----+-----+-----+-----+-----+ 2820
 CCTATCAGTCCTTTTAATACCGAGTTCATACCCACCCGGTTTGGCTTTACACTGACACTG
 D S Q E N Y G S S M G G P N R N V T V T -
 2821 TCAGACTCCTTCCTCAGGAGACTGGGGCTTACCAAACCTCAAAGGCCGGCAGAATGGAACC
 -----+-----+-----+-----+-----+ 2880
 AGTCTGAGGAAGGAGTCTCTGACCCCGAATGGTTTGAGTTTCCGGCCGTCTTACCTTGG
 Q T P S S G D W G L P N S K A G R M E P -
 2881 TATGAATTCAAACCTCCATGGGAAGACCAGGAGGAGATTATAATACTTCTTTACCCAGACC
 -----+-----+-----+-----+-----+ 2940
 AATACTTAAGTTTGAGGTACCCCTTCTGGTCTCTCTAATATTATGAAGAAATGGGTCTGG
 M N S N S M G R P G G D Y N T S L P R P -
 2941 TGCACTGGGTGGCTCTATTCCACATTGCCTCTTCGGTCTAATAGCATACCCAGGTGCGAG
 -----+-----+-----+-----+-----+ 3000
 ACGTGACCCACCGAGATAAGGGGTGTAACGGAGAAGCCAGATTATCGTATGGTCCACGCTC
 A L G G S I P T L P L R S N S I P G A R -
 3001 ACCAGTATTGCAACAGCAGCAGCAGATGCTTCAAATGAGGCCTGGTGAAATCCCCATGGG
 -----+-----+-----+-----+-----+ 3060
 TGGTCATAACGTTGTCGTCGTCGTCTACGAAGTTTACTCCGGACCACTTTAGGGGTACCC
 P V L Q Q Q Q Q M L Q M R P G E I P M G -

FIGURE 1D

[illegible]

FIGURE 1F

G H M G Q M N M N P M P M S G M P M G P -

4321 TGATCAGAAATACTGCTGACATCTCTGCACCAGGACCTCTTAAGGAAACCACTGTACAAA
-----+-----+-----+-----+-----+ 4380
ACTAGTCTTTATGACGACTGAGAGACGTGGTCCTGGAGAATTCCTTTGGTGACATGTTT

D Q K Y C *

4381 TGACACTGCACTAGGATTATIGGGAAGGAATCATTGTTCCAGGCATCCATCTTGGAAGAA
-----+-----+-----+-----+-----+ 4440
ACTGTGACGTGATCCTAATAACCCTTCCTTAGTAACAAGGTCCGTAGGTAGAACCTTCTT

4441 AGGACCAGCTTTGAGCTCCATCAAGGGTATTTTAAGTGATGTCATTTGAGCAGGA
-----+-----+-----+-----+-----+ 4495
TCCTGGTCGAAACTCGAGGTAGTTCCTCCATAAAATTCCTACAGTAAACTCGTCCT

004194-1667060

1 MSGLGENLDP LASDS ^{bHLH domain} SRKRKL PCDTPGQGLT CSGEKRRREQ ESKYIEELAE
 51 LISANLSDID NFNVKPDKCA ILKETVRQIR QIKE ^{PAS 'A' domain} QGKTIS NDDDVQKADV
 101 SSTGQGVIDK DSLGPLLLQA LDGFLFVVNR EANIVFVSEN VTOYLOYKOE
 151 DLVNTSVYNI LHEEDRKDFL KNLPKSTVNG VSWTNEPQRQ KSHTFNCRML
 201 MKTPHDILED INASPEMRQR YETMQCFALS QPRAMMEEGE DLQSCMICVA
 251 RRITTGERTF PSNPES ^{PAS 'B' domain} FITR HDLSGKVVNI DTNSLRSSMR PGFEDIIRRC
 301 IQRFFSLNDG QWSQKRHYQ EAYLNGHA ET PVYRFSLADG TIVTAQTKSK
 351 LFRNPVTNDR HGFVSTHFLQ REQNGYRPNP NPVGQGIRPP MAGCNSSVGG
 401 ^{→ RAC3.1} MSMSPNQGLQ MPSSRAYGLA DPSTTGQMSG ARYGGSSNIA SLTPGPGMQS
 451 PSSYQNNNYG LNMSSPPHGS PGLAPNQONI MISPRNRGSP KIASHQFSPV
 501 AGVHSPMASS GNTGNHSFSS SLSALQAIS EGVGTSLLST LSSPGPKLDN
 551 SPNMNITQPS KVSNQDSKSP LGFYCDQNPV ESSMCQNSNR DHLSDKESKE
 601 SSVEGAENQR GPLESKGHKK ⁱ LLQLITCSSD DRGHSSLTNS PLDSSCKESS
 651 VSVTSPSGVS SSTSGGVSST SNMHGSLLOE ⁱⁱ KHRLLHKLLO NGNSPAEVAK
 701 ITAEATGKDT SSITSCGDGN VVKQEQLSPK ⁱⁱⁱ KKENNALRLRY LLDRDDPSDA
 751 LSKELQPQVE GVDNKMSQCT SSTIPSSSQE KDPKIKTETS EEGSGDLNLDN
 801 ^{iv} DAILLGDLTSS DFYNNSISSN GSHLGTKQQV FQGTNSLGLK SSQSVQSIRP
 851 PYNRAVSLDS PVSVGSSPPV KNISAFPMPLP KQFMLGGNPR MMDSQENYGS
 901 SMGGPNRNVV VTQTPSSGDW GLPNSKAGRM EPMNSNSMGR PGGDYNTSLP
 951 RPALGGS IPT LPLRSNSIPG ARPVLQQQQQ MLQMRPGEIP MGMGANPYGQ
 1001 AAASNQLGSW PDGMLSMEQV SHGTQNRPLL RNSLDDL VGP PSNLEGQSDE
 1051 ^v RALLDQLHTL LSNTDATGLE ^{vi} EIDRALG IPE LVNQQALEP KQDAFQGQEA
 1101 AVMMDQKAGL YGQTYPAQGP PMQGGFHLQG QSPSFNSMMN QMNQQGNFPL
 1151 QGMHPRANIM ^{Q-rich domain} RPRNTNPKQL RMQLQORLOG QOFLNQSROA LELKMNPTA
 1201 ^{← RAC3.1} GGAAVMRPMM QPQOGFLNAQ MVAQRSRELL SHHFROORVA MMMQQQQQQQ
 1251 QQQQQQQQQQ QQQQQQQQQT QAFSPPPNVT ASPSMGLLA GPTMPQAPPQ
 1301 QFPYQPNYGM GQQPDPAFGR VSSPPNAMMS SRMGPSQNPM MQHPQAASIY
 1351 QSSEMKGWPS GNLA RNSSFS QQQFAHQGNP AVYSMVHMNG SSGHMGQMNM
 1401 NPM PMSGMPM GPDQKYC*

FIGURE 2

06041694-031398

i.	SKGHKK	LLQLL	TCSSDD	RAC3	(615-631)
	SKGQTK	LLQLL	TTKSDD	TIF2	(840-651)
	SQTSHK	LVOLL	TTTAAE	SRC1	(632-643)
ii.	LQEKHR	ILHKLL	QNGNSP	RAC3	(678-695)
	LKEKHK	ILHRLL	QDSSSP	TIF2	(683-699)
	LTERHK	ILHRLL	QEG.SP	SRC1	(683-699)
iii.	KKKE...	NNALLRYLL	DRDDPSD	RAC3	(730-749)
	KKKE...	NNALLRYLL	DKDDTKD	TIF2	(738-753)
	KKKESKD	HQLLRYLL	DKDE.KD	SRC1	(739-757)
iv.	DLDNLDA	ILGDL		RAC3	(796-807)
	ELDNLEE	ILDDL		TIF2	(803-814)
	DLDQFDQ	LLPTL		SRC1	(810-821)
v.	EGQSDERA	LLDQL	HTLL	RAC3	(1045-1061)
	ESPSDEGA	LLDQL	YLAL	TIF2	(1071-1087)
	EGRNDEKA	LLDQL	VSFL	SRC1	(924-940)
vi.	LEEIDRALG	IPELV	NQ	RAC3	(1069-1084)
	LEEIDRALG	IPELV	SQ	TIF2	(1093-1108)
	LAELDRALG	IDKLV	.Q	SRC1	(948-962)
vii.	QTPQAQKS	LLQQL	UTE*	SRC1	(1424-1440)

FIGURE 4

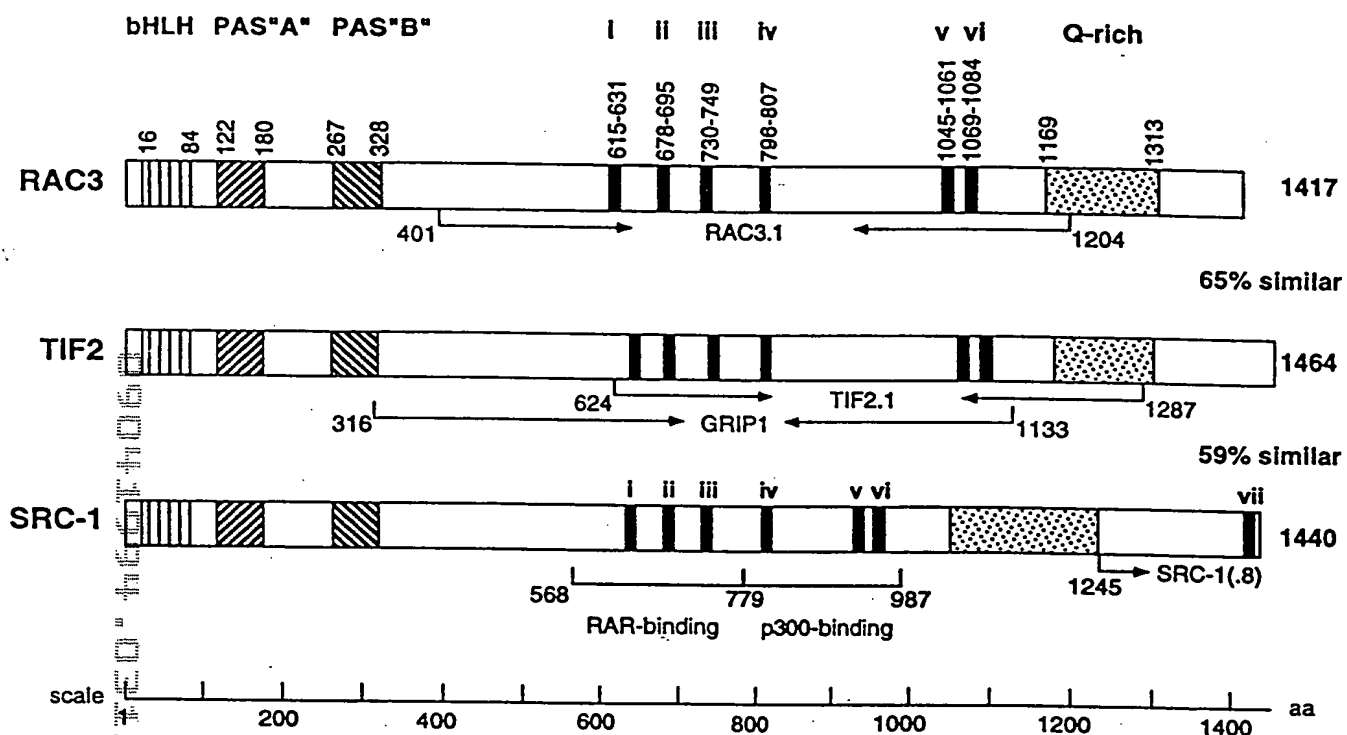


FIGURE 5

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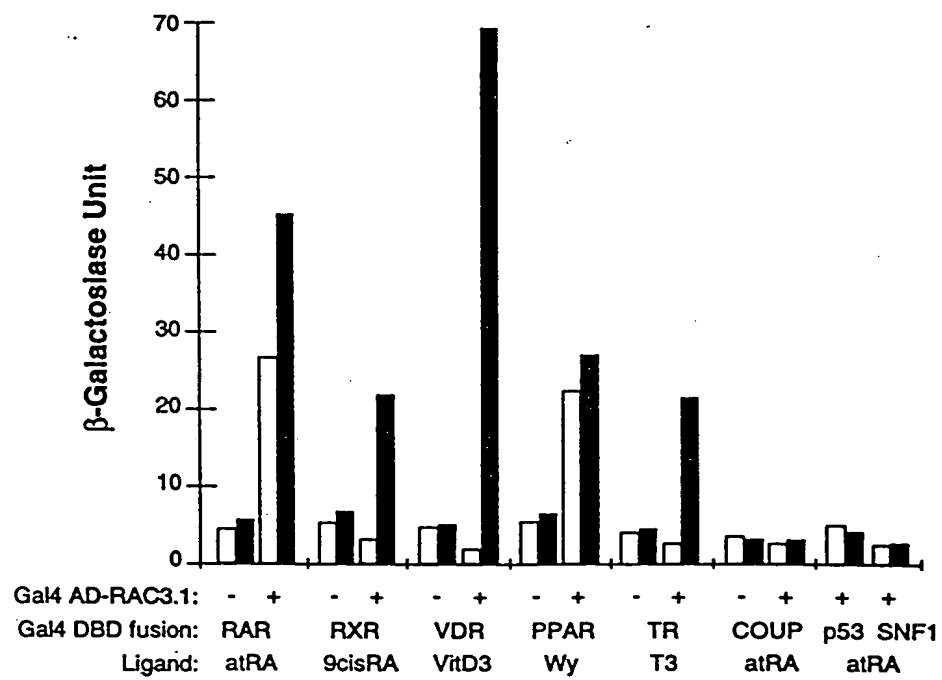


FIGURE 6

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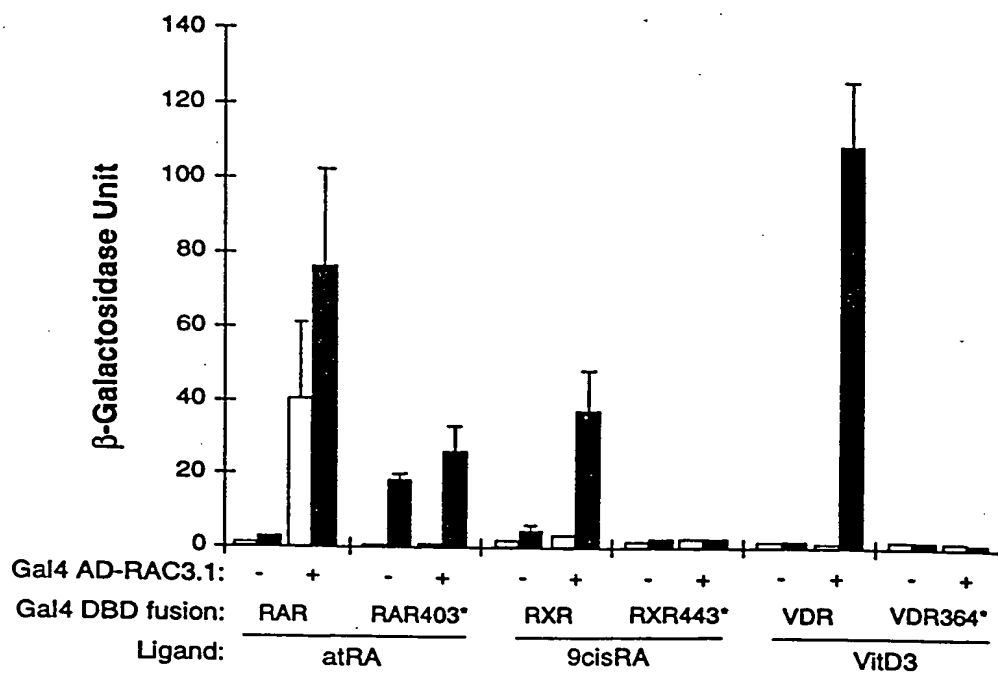


FIGURE 7

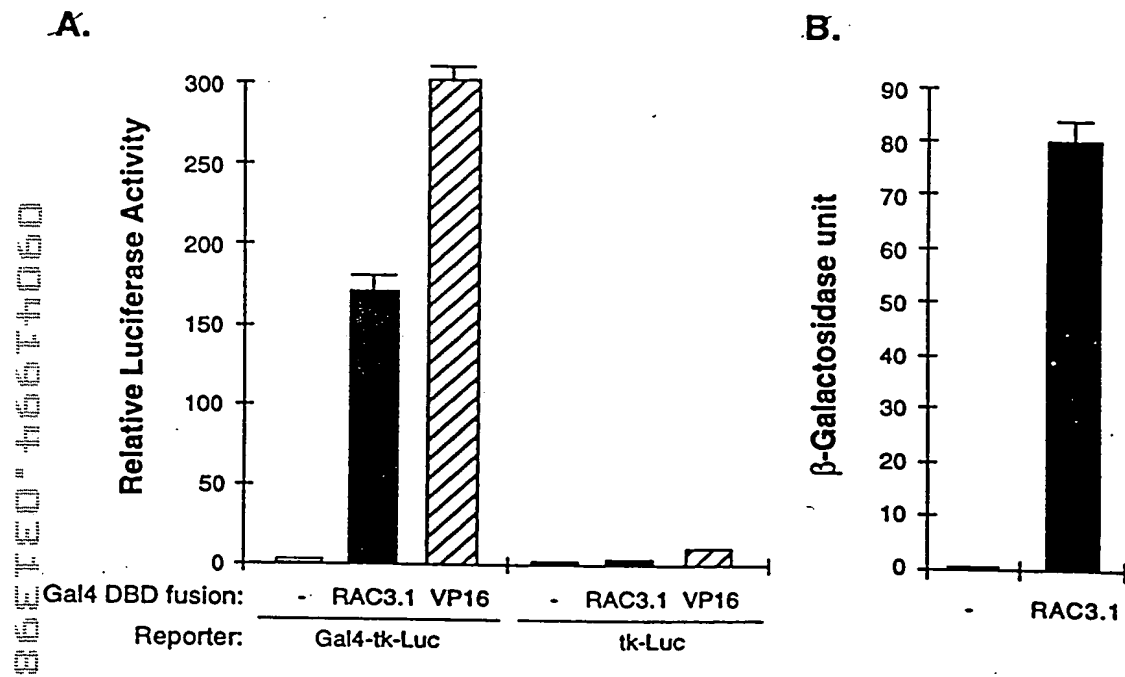


FIGURE 8

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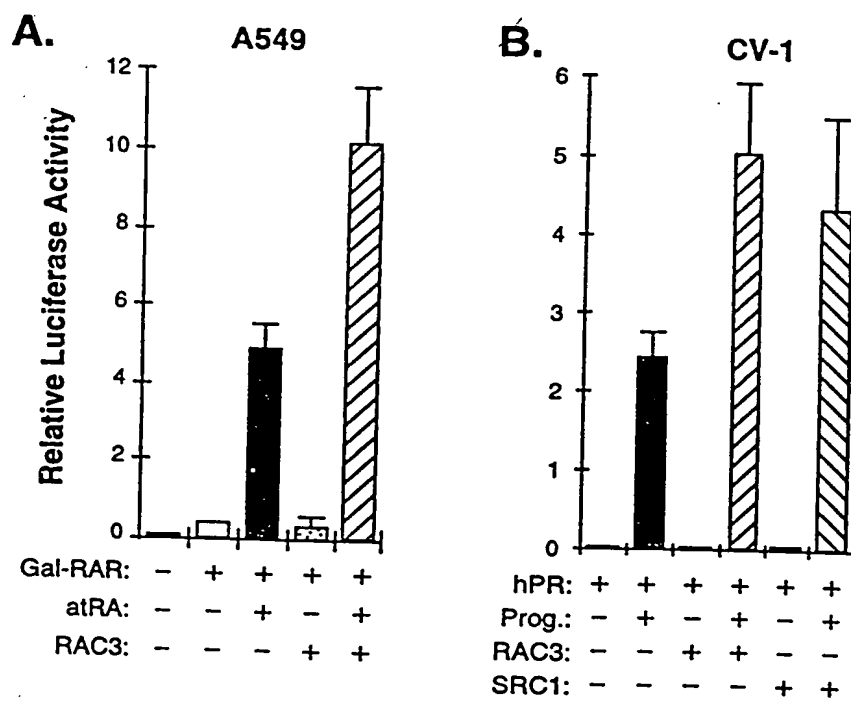


FIGURE 9